

PCT09

ENTERE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/830,706B

DATE: 04/22/2002

TIME: 15:01:38

Input Set : A:\55865sequence.txt

Output Set: N:\CRF3\04222002\1830706B.raw

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4 <110> APPLICANT: TOJI, SHINGO
             YANO, MINORU
             TAMAI, KATSUYUKI
     8 <120> TITLE OF INVENTION: THIOREDOXIN REDUCTASE II
     10 <130> FILE REFERENCE: 55865-71965
   12 <140> CURRENT APPLICATION NUMBER: 09/830,706B
C-->13 <141> CURRENT FILING DATE: 2002-01-29
   15 <150> PRIOR APPLICATION NUMBER: PCT/JP99/05983
   ii16 <151> PRIOR FILING DATE: 1999-10-28
   18 <150> PRIOR APPLICATION NUMBER: JP 1998-310422
     19 <151> PRIOR FILING DATE: 1998-10-30
   21 <160> NUMBER OF SEQ ID NOS: 38
   23 <170> SOFTWARE: PatentIn Ver. 2.1
   25 <210> SEQ ID NO: 1
   # 26 <211> LENGTH: 1959
   27 <212> TYPE: DNA
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   31 <221> MARIE, NEI. 32 <222> LOCATION: (10)..(1572) 34 <220> FEATURE:
   35 <221> NAME/KEY: misc_feature
     36 <222> LOCATION: (1567)..(1569)
     37 <223> OTHER INFORMATION: "tga" is translated to selenocysteine
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                   1
                                                                          99
     45 Arg Thr Gln Ala Val Ala Gly Gly Val Arg Gly Ala Ala Arg Gly Ala
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                                                                          147
     48 gca gca ggt cag cgg gac tat gat ctc ctg gtg gtc ggc ggg gga tct
     49 Ala Ala Gly Gln Arg Asp Tyr Asp Leu Leu Val Val Gly Gly Gly Ser
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                        35
     52 qqt qqc ctq qct tqt qcc aaq gag gcc gcc cag ctg gga agg aag gtg
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     53 Gly Gly Leu Ala Cys Ala Lys Glu Ala Ala Gln Leu Gly Arg Lys Val
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                    50
                                                                          243
     56 gcc gtg gtg gac tac gtg gaa cct tct ccc caa ggc acc cgg tgg ggc
     57 Ala Val Val Asp Tyr Val Glu Pro Ser Pro Gln Gly Thr Arg Trp Gly
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    60 ctc ggc ggc acc tgc gtc aac gtg ggc tgc atc ccc aag aag ctg atg
    61 Leu Gly Gly Thr Cys Val Asn Val Gly Cys Ile Pro Lys Lys Leu Met
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	att	αac	gag	cac	аса	αt t	tac		att	acc	aaa	aat		aaa	σασ	att	531
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82	, u _	160	Olu			,	165	011				170		_10	0_0		
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97 198 100 101	Ala ctg Leu	Ser gac Asp	Tyr 225 acc Thr	Val acc	Ala atc	Leu atg	Glu atg Met	Cys 230 cgc Arg	Ala ago	Gly ato	Phe ccc	Leu cto Leu	Thr 235 cgc Arg	Gly ggc	Ile tto	Gly	
197 198 100 101 102	Ala ctg Leu	Ser gac Asp 240	Tyr 225 acc Thr	Val acc Thr	Ala atc Ile	Leu atg Met	Glu atg Met 245	Cys 230 cgc Arg	Ala ago Ser	Gly ato	Phe ccc Pro	Leu cto Leu 250	Thr 235 cgc Arg	Gly ggc Gly	Ile tto Phe	Gly gac Asp	771
97 98 100 101 102	Ala ctg Leu cag	Ser gac Asp 240	Tyr 225 acc Thr atg	Val acc Thr	Ala atc Ile tcc	Leu atg Met	Glu atg Met 245	Cys 230 cgc Arg ata	Ala agc Ser gag	Gly ato Ile	Phe ccc Pro atg	Leu cto Leu 250 gca	Thr 235 cgc Arg	Gly ggc Gly	Ile tto Phe	Gly gac Asp	
97 198 100 101 102 104	Ala ctg Leu cag	Ser gac Asp 240 caa	Tyr 225 acc Thr atg	Val acc Thr	Ala atc Ile tcc	Leu atg Met	Glu atg Met 245 gtc Val	Cys 230 cgc Arg ata	Ala agc Ser gag	Gly ato Ile	Phe ccc Pro atg	Leu cto Leu 250 gca Ala	Thr 235 cgc Arg	Gly ggc Gly	Ile tto Phe	Gly gac Asp	771
97 198 100 101 102 104 105	Ala ctg Leu cag Gln 255	Ser gac Asp 240 caa Glr	Tyr 225 acc Thr atg	acc Thr tcc Ser	atc Ile tcc Ser	Leu atg Met atg	Glu atg Met 245 gtc Val	Cys 230 cgc Arg ata Ile	agc Ser gag Glu	Gly atc lle cac	Phe ccc Pro atg Met 265	Leu ctc Leu 250 gca Ala	Thr 235 cgc Arg tct	Gly ggc Gly cat	Ile tto Phe ggo	Gly gac Asp acc	771
97 98 100 101 102 104 105 106 108	Ala ctg Leu cag Gln 255	Ser gac Asp 240 caa Glr	Tyr 225 acc Thr atg	acc Thr tcc Ser	atc Ile tcc Ser	Leu atg Met atg Met 260	Glu atg Met 245 gtc Val	Cys 230 cgc Arg ata Ile	agc Ser gag Glu	Gly atc Ile cac His	Phe ccc Pro atg Met 265 gtc	Leu ctc Leu 250 gca Ala	Thr 235 cgc Arg tct Ser	Gly ggc Gly cat His	Ile tto Phe ggo Gly	gac Asp acc Thr 270	771 819
97 98 100 101 102 104 105 106 108 109	Ala ctg Leu cag Gln cgg Arg	gac Asp 240 caa Glr tto	Tyr 225 acc Thr atg Met	acc Thr tcc Ser agg Arg	atc Ile tcc Ser ggc Gly 275	Leu atg Met atg Met 260 tgt	Glu atg Met 245 gtc Val gcc	Cys 230 cgc Arg ata Ile ccc Pro	agc Ser gag Glu tcg Ser	Gly atc Ile cac His cgg Arg 280	Phe ccc Pro atg Met 265 gtc Val	Leu ctc Leu 250 gca Ala agg	Thr 235 cgc Arg tct Ser agg	Gly ggc Gly cat His	The tto Phe ggo Gly cct Pro 285	Gly gac Asp acc Thr 270 gat Asp	771 819 867
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197 2100 100 101 102 104 105 106 108 110 112 113	Ala ctg Leu cag Gln cgg Arg	ser gac Asp 240 caa Glr ttc	Tyr 225 acc Thr atg Met ctg	acc Thr tcc Ser agg Arg cag	atc Ile tcc Ser ggc Gly 275 gtc	Leu atg Met 260 tgt Cys	Glu atg Met 245 gtc Val gcc Ala	Cys 230 cgc Arg ata Ile ccc Pro	ago Ser gag Glu tcg Ser gac Asp	Gly atc atc cac His cgg Arg 280 agc Ser	Phe ccc Pro atg Met 265 gtc Val	Leu ctc Leu 250 gca Ala agg Arg	Thr 235 cgc Arg tct Ser agg	Gly ggc Gly cat His ctc Leu aag	The tto Phe ggo Gly cct Pro 285 gag	Gly gac Asp acc Thr 270 gat Asp	771 819 867
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97 108 100 101 105 106 108 109 110 111 113 114 116 117 118 120	Ala ctg Leu cag Gln cyg Ggc Gly acg Thr	gac Asp 240 caa Glr tto Phe Glr ggo	Tyr 225 acc Thr atg tell ctg Leu ctg Thr 305 agt	val acc Thr tcc Ser agg Arg Cag Gln 290 ttt Phe	atc Ile tcc Ser ggc Gly 275 gtc Val gac Asp	atg Met 260 tgt Cys acc Thr	Glu yatg Atg Yatc Yal yacc Ala tgg Trp yacc Yal	Cys 230 cgc Arg ata Ile ccc Pro gag Glu ctg Leu 310 aag	age Ser gag Glu teg Ser gac Asp 295 tgg Trp	cac His Cgg Arg 280 agc Ser ggg	Phe ccc Pro atg Met 265 gtc Val acc Thr ata Ile	Leu ctc Leu 250 gca Ala agg Arg acc Thr	Thr 235 cgc Arg tct Ser agg Arg Gly cga Arg 315 act	Gly ggc Gly cat His ctc Leu aag Val	ttc Phe ggc Gly cct Pro 285 gag Glu	gac Asp acc Thr 270 gat Asp gac Asp	771 819 867 915
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205			35					40					45			
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213	Gly	Thr	Cys	Val	Asn	Val	Gly	Cys	Ile	Pro	Lys	Lys	Leu	Met	His	Gln
214					85					90					95	
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219	Glu	Val	Ala	Gln	Pro	Val	Pro	His	Asp	Trp	Arg	Lys	Met	Ala	Glu	Ala
☐ 220			115					120					125			
222	Val	Gln	Asn	His	Val	Lys	Ser	Leu	Asn	Trp	Gly	His	Arg	Val	Gln	Leu
A 223		130				-	135			_	_	140				
225 ليا	Gln	Asp	Arq	Lys	Val	Lys	Tyr	Phe	Asn	Ile	Lys	Ala	Ser	Phe	Val	Asp
<u></u>		-	_	-		150	-				155					160
228		His	Thr	Val	Cys	Gly	Val	Ala	Lys	Gly	Gly	Lys	Glu	Ile	Leu	Leu
= 229					165	-			-	170	_	_			175	
231	Ser	Ala	Asp	His	Ile	Ile	Ile	Ala	Thr	Gly	Gly	Arg	Pro	Arg	Tyr	Pro
232			•	180					185	-	-			190	-	
234	Thr	His	Ile	Glu	Gly	Ala	Leu	Glu	Tyr	Gly	Ile	Thr	Ser	Asp	Asp	Ile
2 35			195		-			200	•	-			205	-	-	
P 237	Phe	Trp	Leu	Lys	Glu	Ser	Pro	Gly	Lys	Thr	Leu	Val	Val	Gly	Ala	Ser
2 38		210		*			215	•	-			220		-		
240	Tvr	Val	Ala	Leu	Glu	Cys	Ala	Gly	Phe	Leu	Thr	Gly	Ile	Gly	Leu	Asp
241	_					230		-			235	-		-		240
243	Thr	Thr	Ile	Met	Met	Arq	Ser	Ile	Pro	Leu	Arg	Gly	Phe	Asp	Gln	Gln
244					245	_				250	_	-		_	255	
246	Met	Ser	Ser	Met	Val	Ile	Glu	His	Met	Ala	Ser	His	Gly	Thr	Arg	Phe
247				260					265				_	270	-	
249	Leu	Arg	Gly	Cys	Ala	Pro	Ser	Arg	Val	Arg	Arg	Leu	Pro	Asp	Gly	Gln
250		_	275	-				280		_	_		285	_	_	
252	Leu	Gln	Val	Thr	Trp	Glu	Asp	Ser	Thr	Thr	Gly	Lys	Glu	Asp	Thr	Gly
253		290			-		295				_	300		_		_
255	Thr	Phe	Asp	Thr	Val	Leu	Trp	Ala	Ile	Gly	Arg	Val	Pro	Asp	Thr	Arg
	305		-			310	-			_	315			_		320
258	Ser	Leu	Asn	Leu	Glu		Ala	Gly	Val	Asp	Thr	Ser	Pro	Asp	Thr	Gln
259					325	•		-		330				_	335	
	Lys	Ile	Leu	Val	Asp	Ser	Arq	Glu	Ala	Thr	Ser	Val	Pro	His	Ile	Tyr
262	•			340	•		_		345					350		_
264	Ala	Ile	Gly		Val	Val	Glu	Gly	Arq	Pro	Glu	Leu	Thr	Pro	Thr	Ala
265			355	-				360	_				365			
	Ile	Met		Gly	Arg	Leu	Leu	Val	Gln	Arg	Leu	Phe	Gly	Gly	Ser	Ser
268		370		-	_		375					380	_	_		
	Asp	Leu	Met	Asp	Tyr	Asp	Asn	Val	Pro	Thr	Thr	Val	Phe	Thr	Pro	Leu
	385			-	-	390					395					400

RAW SEQUENCE LISTING DATE: 04/22/2002 PATENT APPLICATION: US/09/830,706B TIME: 15:01:38

Input Set : A:\55865sequence.txt

Output Set: N:\CRF3\04222002\1830706B.raw

```
273 Glu Tyr Gly Cys Val Gly Leu Ser Glu Glu Glu Ala Val Ala Arg His
                         405
                                             410
    274
    276 Gly Gln Glu His Val Glu Val Tyr His Ala His Tyr Lys Pro Leu Glu
    277
                     420
                                         425
    279 Phe Thr Val Ala Gly Arg Asp Ala Ser Gln Cys Tyr Val Lys Met Val
                                                         445
                                     440
                 435
    282 Cys Leu Arg Glu Pro Pro Gln Leu Val Leu Gly Leu His Phe Leu Gly
                                 455
    285 Pro Asn Ala Gly Glu Val Thr Gln Gly Phe Ala Leu Gly Ile Lys Cys
    286 465
                             470
                                                 475
    288 Gly Ala Ser Tyr Ala Gln Val Met Arg Thr Val Gly Ile His Pro Thr
                                             490
                                                                  495
                        485
    291 Cys Ser Glu Glu Val Val Lys Leu Arg Ile Ser Lys Arg Ser Gly Leu
                    500
                                         505
W-- 294 Asp Pro Thr Val Thr Gly Cys Xaa Gly
    295
                 515
  298 <210> SEQ ID NO: 3
   299 <211> LENGTH: 2056
   □300 <212> TYPE: DNA
   🖼 301 <213> ORGANISM: Homo sapiens
   □303 <220> FEATURE:
   〒304 <221> NAME/KEY: CDS
   305 <222> LOCATION: (188)..(1669)
   __307 <220> FEATURE:
    308 <221> NAME/KEY: misc_feature
     309 <222> LOCATION: (1664)..(1666)
   310 <223> OTHER INFORMATION: "tga" is translated to selenocysteine
   312 <400> SEQUENCE: 3
   🔤 313 gtcccggacc tcaggcccag ttcagtgtac ttcccctctc tacttcctcc ctccagtccc 60
   #315 ttctccatcc ctcccttttt tggctgcccc ttgcctgcct tcctcgccag tagcttgcag 120
    317 agtaqacacq atqacacctt ttgcaggcta aaaaggctga gagtggcact atgtgcagtg 180
    319 agccacc atg gag gac caa gca ggt cag cgg gac tat gat ctc ctg gtg
    320
                Met Glu Asp Gln Ala Gly Gln Arg Asp Tyr Asp Leu Leu Val
    321
    323 gtc ggc ggg gga tct ggt ggc ctg gct tgt gcc aag gag gcc gcc cag
                                                                            277
    324 Val Gly Gly Gly Ser Gly Gly Leu Ala Cys Ala Lys Glu Ala Ala Gln
                             20
                                                  25
                                                                            325
    327 ctg gga agg aag gtg gcc gtg gtg gac tac gtg gaa cct tct ccc caa
    328 Leu Gly Arg Lys Val Ala Val Val Asp Tyr Val Glu Pro Ser Pro Gln
                         35
    331 ggc acc cgg tgg ggc ctc ggc ggc acc tgc gtc aac gtg ggc tgc atc
                                                                            373
    332 Gly Thr Arg Trp Gly Leu Gly Gly Thr Cys Val Asn Val Gly Cys Ile
                     50
                                                              60
    335 ccc aag aag ctg atg cac cag gcg gca ctg gga ggc ctg atc caa
                                                                            421
    336 Pro Lys Leu Met His Gln Ala Ala Leu Leu Gly Gly Leu Ile Gln
    339 gat gcc ccc aac tat ggc tgg gag gtg gcc cag ccc gtg ccg cat gac
    340 Asp Ala Pro Asn Tyr Gly Trp Glu Val Ala Gln Pro Val Pro His Asp
    341
                                  85
             80
```

<u>ngempre neovol</u>

RAW SEQUENCE LISTING ERROR SUMMARY PATENT APPLICATION: US/09/830,706B

DATE: 04/22/2002 TIME: 15:01:39

Input Set : A:\55865sequence.txt

Output Set: N:\CRF3\04222002\1830706B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 520
Seq#:2; Xaa Pos. 520
Seq#:3; Xaa Pos. 493
Seq#:4; Xaa Pos. 493
Seq#:37; N Pos. 31417
Seq#:38; Xaa Pos. 498



VERIFICATION SUMMARY

PATENT APPLICATION: US/09/830,706B

DATE: 04/22/2002 TIME: 15:01:39

Input Set : A:\55865sequence.txt

Output Set: N:\CRF3\04222002\1830706B.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1592 L:294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:512 L:440 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:1669 L:559 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:480 L:2002 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:31380 L:3281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:496